Evaluation of a multiparametric qBOLD approach in patients with brain tumors

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Introduction
In clinical monitoring of brain tumors, Perfusion Weighted Imaging (PWI) contributes to tumor grading and to assess the response to treatment, as early as possible [1]. Beyond tumor perfusion, tumor hypoxia has been shown to determine the response of various therapeutic approaches including radiotherapy. The aim of this study is to evaluate in patients how tissue oxygen saturation (StO2), assessed with a multiparametric qBOLD approach [2], could contribute to characterize brain tumors using a model-based cluster approach.

Materials and Methods
Groups. Thirteen subjects (7 males/6 females) with untreated brain tumor were examined after written informed consent was obtained (approved by local IRB). Group was composed of 5 glioblastomas, 2 metastases, 1 meningioma, 2 astrocytomas, 1 gliomatosis, 1 ependymoma, 1 oligodendroglioma.

Acquisition. The imaging protocol was carried out on a 3T TX Achieva MR scanner (Philips Healthcare®) using a whole-body RF transmit and 8-channel head receive coils. Three sequences were acquired with a FOV of 224x20x184mm: a 3D multi gradient echo (GE) sequence related to “healthy” voxels. All the 13 patients in all the brain parenchyma. Normal mixture modeling was performed on voxel data using Expectation-Maximization algorithms implemented in the R package mclust [3]. Model choice and the optimal number of clusters (k=7 clusters) were determined with a Bayesian information criterion [3].

Data Analysis. As described in the literature [2], StO2 maps were obtained pixelwise from a combination of CBV and T2, where 1/T2' = 1/T2* - 1/T2 and using a hematocrit of 0.4; T2 and T2* maps were calculated by fitting a monoexponential decay to the corresponding MR images. A map of Cerebral Metabolic Rate of oxygen (CMRO2) was computed using CMRO2 = CBF x (1-StO2/100). Eventually, a model-based cluster analysis was performed on voxels obtained from the 13 patients in all the brain parenchyma. Normal mixture modeling was performed on voxel data using Expectation-Maximization algorithms implemented in the R package mclust [3]. Model choice and the optimal number of clusters (k=7 clusters) were determined with a Bayesian information criterion [3].

Results

Figure 1. 3DT1-Gd (a), CBV (b), CBF(c), MTT (d) StO2 (e) CMRO2 maps (f) and model-based cluster analysis (g) from one patient with glioblastoma.

Fig. 1 shows representative parametric maps obtained from one patient. The model-based cluster analysis (Fig.1g) of 7 clusters shows that white matter composed of the same cluster (pink), which can thus be related to “healthy” voxels. All the parameters in the clusters 1 and 2 are lower than other clusters and correspond to cerebrospinal fluid except in the tumor or its probably necrosis. The yellow cluster is similar to the orange cluster but has higher CBV, CBF and CMRO2 (Fig 2). The red cluster corresponds to gray matter component. Tumor is heterogeneously composed of 4 clusters (black, orange, purple and red) but mainly composed of the purple cluster for which the mean transit time is increased. A gadolinium-enhanced scan (Fig 1a) shows active lesion, meaning that there is a degradation of the vascular wall integrity explaining the increase in the mean transit time.

Discussion / Conclusion
This study on brain tumor oxygenation is the first report of StO2 obtained with MRI. StO2 and CMRO2 seem to provide new information that could contribute to tumor grading and tumor hypoxia evaluation. Cluster analysis can be used to structure the wealth of information gathered with multiparametric microvascular MRI. The cluster-based analysis highlights several types of physiological behavior, which could correspond to different level of the tumor evolution. A cluster-based analysis of the tumor microvascular characteristic has a great potential to ease tumor diagnosis, prognosis, and treatment follow-up.

References